STIC-Biotech/ChemLib

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From	
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Borin, Michael

Sent: To:

Tuesday, February 26, 2002 1:59 PM STIC-Biotech/ChemLib Search request: 09/540325

Subject:

Examiner: M.Borin CM1 12A01

AU: 1631; Mailbox 12D01

Tel.: 305-4506

RE: 09/540325; cyanidium nucl. acids



Please conduct search of polynucleotide SEQ ID 1 against the commercial and interference databases.

Thank you

Searcher: Paula Shoppad
Searcher: Paule Shopped Phone: 308-4499
Location:
Date Picked Up: 3/02/02
Date Completed: 3/04/64
Searcher Prep/Review: 10
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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 GenEmbl:*
1: gb_ba:*
2: gb_htg:
3: gb_in:*
4: gb_ow:*
6: gb_pov:*
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8: gb_pr:
10: gb_r:
11: gb_s:
12: gb_s:
12: gb_u
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15: em_l
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

JOURNAL	AUTHOR TITLE	ORGANI:	SOURCE	RESULT 1 AB013390/c LOCUS DEFINITION ACCESSION VERSION		44 45	c 43	c 41	ωι	C 36	0	ωω; ωω;	2 3 1 2 1	29 30	27 28	25 26	c 23	21 22	19 20	17 18	15 16	14	112	10 11	o တ		c 5 4	- ω	c 1 2	Result
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., Sato,S., Asamizu,E., Ka if Arabidopsis thaliana chr the regions of 1,367,185 b 11 and TAC clones 16 (1998)	tae; Streptophyta; Embryop iophyta; eudicotyledons; c Brassicales; Brassicaceae	(strain:Columbia) DNA, cl	DNA PLN genomic DNA, chromosome 5	ALIGNMENTS	AC012498 LMFLCHR36_22	AC008391 AC078817	AC079871 AC016618	AC026478	MML26MRN AC022431	CNS06JUZ	AP002913	HUMRPL26X	YSCL8300 U67497	RRRPL26 AX073088	AC091012 AC026645	HSAC001236 AC002536	CNS019VN D78495	CNS01CH1 SCYGR034W	CNS01CVL CNS01D4C	CNS01BT1 CNS01COM	CNS019FV	CNS01CFH CNS0197Z	CNS01B90	CNS06IDT	SPBC29B5 AC091511	YSP972HB	ATT16K5	AB013390 AF370158	ID	
очегеа ру	neko,T., Miyaj omosome 5. VI.	phyta; Tracheophyta; core eudicots; e; Arabidopsis.	clone_lib:Mitsui TAC	27-DEC-2000 , TAC clone:K919.		omo sap on (23	omo sap	musc o sap	omo sap	musculu omo sap	AL402081 T7 end of	ryza sa	L07287 Human ribos	charomy	t liver		AC001236 Homo sapi AC002536 Human Chr	otryt	AL115517 Botrytis 272819 S.cerevisia	AL116041 Botrytis AL116356 Botrytis	AL114653 Botrytis AL115790 Botrytis	ALII194/ BOTTYTIS AL113186 Botrytis	AL111303 Botrytis	AL113932 Botrytis	AL400167 T7 end of	. pomb	sion ye	L132965 Arabidop	13390 Arabido 70158 Arabido	Description

KMEKQSKKDESRWKLLVKNVLGSKKIGGSPFFLPVTNC"
complement(join(13074..13266,13326..1
/note="gene_id:K919.5 SVIIEANTRKERMRKRNDQRIYSQLYEAMEALVHICRDGCKTIGPHDKDFKPNHATCN YEACKGLESLIRHFAGCKLRVPGGCVHCKRMWQLLELHSRVCAGSDQCRVPLCRNLKE /translation="MVTGCVDLHQSFKSADSSSVPIPPPLPSKSDGLKKKLGHSSVST ATRDMWDRLFNDGYKADVVIYTDNGSIIYAHANILGTASTVIKGMLKQAKRHGKWHTI SIRGVPHDAVRVFIRFLYSSCYEKEENNEFINHLLLLSHAYVVPQLKRVCEWHLEHGL VDIKGVDGKTTLLHFVVQEITRSEGTTTTKDETILHGNNDGFRKQGLQVVAGLSRDLV NVKKSAGMDFDVLSSYVTKLEMGLDKLRSFLKTETTQGRFFDSMKTFLKEAEEEIRKI KGGERKALSMVKEVTEYFHGNAAREEAHPLRIFMVVRDFLGVLDNVCKEVKTMQEMST SMGSASARSFRISATASLFVLHRYKARQDDTSSDSEHSSNSST" /translation="MSKGPGLFTDIGKKAKDLLTRYNSDQKFSISYYSASGYALTST ALKKGGYHAADVATQKYKNALFDVKLDTDSSYLTTVTLTEILPSTKAIASFKVPDXN SAKLEVQYFHDHATVTAAAALKQNPLLDITATLGSPVLSFGAEAGYDTTSKTFTKYNA GISVTKPDACLSIILGDKGDSLKASYLHHFDEFKRTAAVGEVYRKFSTNENTTTVGGL /translation="matnnivrliapsrsyssrflepvsrflssgtpppppqapspnqd LNRDVKPDQNLQQNLQMQKEEEEEGEGGGGGEFVNEDTGEIGGPRGPEPTRYGDWEQR ACSYIFLGKMEINSFYVFMYLQNNGENGRKCSRTSNSLPLFGSSFSGDLVIPVIVNKF /evidence=not_experimental /protein_id="BAB08457.1" /db_xref="GI:9757870" unknown protein" /evidence=not_experimental /protein_id="BAB08456.1" /db_xref="GI:9757869" strong similarity to pir||T04718 11426. complement(join(10221. .10664,10740. .11046,11155. .11285 VKYLRNSFQTLEEASLELKASRLFLKLLEAVLMTGNRMNVGTNRGDATAFKLDTLLKL /translation-"MARCVGRCYVSDAFGESESSHLSERRFIKLSSSTNSDPAGSKSL KLRGKIHRRMSYFRPIMAKDESISSRSGETKQINGKOKNIVWHDCPVTKSDRQELIKQ KGCVUMITGLISGSGKGSLACALISALHNRGKLSYILDGDNVHIGLNSDLSFEADDRAE NIRRVGEVAKLFADSGIICIASLISPYRIERAACRALLPQGDFIEVFMDVPLHVCEAR RSMPIRKDDEVQVVRGTFKGREGKVMQVYRKKWVIHIERITHEKVNGSTVNVGVNASN VMITKLRLDKDRKSLLERKANGRAADKEKGTKFSAEDVMENVD" 19478. .1950 join (18523 . 18736 , 18919 . 19050, 19138 . .19406, 19478 . .1950 19698 . .19766, 19905 . .20008) /evidence=not_experimental
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Ecker, J.R.

Seki, M.,

Kawai,J.,

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RESULT
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                                                                  AF370158 729 bp mRNA PLN 3
Arabidopsis thaliana putative 60S ribosomal protein
(T16K5.260/AT3g49910) mRNA, complete cds.
                AF370158
AF370158.1
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KPIPLVEEFLDDKSPIRHLFFPGIKTAAFGPTKDMGNETSYYFPGKIWMDTQGNPIQA
HGGGILLDVKSNTYYWYGEYKDGPTYHAHKKGPARVDIIGVGCYSSKDLWTWKNEGIV
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DSDISTIGVSKKRKTTASASTGFKDFSSW"
complement(join(33419. .24249,24339. .24923))
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MIQGGDPTGTGKGGESIWGKPFKDEPNSKLLHSGRGVVSMANSGPHTNGSQFFVLYKS
ATHLNYKHTVFGGVVGGLATLAAMENVPVDESDRPLEEIKIIEASVFVNPYTELDEEE
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VMVGQHREAPAIFKHQNIYYMVTSWCTGWAPNEALAHAAESIMGPWEKLGNPCIGGNK
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out the Salk, Stanford, PGEC (SSP) Consortium members carried out the Sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S.X Sakano, H., Pham, P.K., Banh, J., Croimmi, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-APR-2001) Plant Gene Expression Center, 800 Bu Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and
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Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu
Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
Tokan, T. Tori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                    /gene="T16K5.260/AT3g49910"
713
                                                                                             /translation="MKYNPRVTSSRRKNRKAHFTASSSERRVIMSSPLSTDLRQKYNVRSMPIRKDDEVQIVRCTYKGREGKVVQVYRRKWVIHIERITREKVNGTTVNVGIQPSKVVITKLRLDKDRKSLLERKAKGRAAADKEKGTKFTSEDVMQNVD"
497. 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="This clone is in a modified
(Lambda ZAP) as a XhoI/SstI insert
ecotype: Columbia"
                                                                                                                                                                                                                                                   /evidence=experimental
/product="putative 60S ribosomal protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T16K5.260/AT3g49910"
56. .496
                                                                                                                                                                                                                                                                                                                                                /gene="T16K5.260/AT3g49910"
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                                                                                                                                                                                                                           /db_xref="GI:13877791"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="T16K5.260/AT3g49910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RAFL05-09-M22 (R10145)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana'
/db_xref="taxon:3702"
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Ishida, J.,

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AL132965
                                                                                                                    Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/Location/Qualifiers
                                                                                                                                                                                                                                 submitted (19-JAN-2000) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-m Lemcke@mips.blochem.mpg.deproject Coordinator: Marcel Salanoubat and Francis Quetier, Groupemen
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                     d'Interet Public, Centre National de Sequencage
Gaston Cremieux, BP191, 91006 Evry Cedex, France
                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing, project.
Direct Submission
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 3442.
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                                          /db_xref="taxon:3702"
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                                                                            /organism="Arabidopsis
/variety="Columbia"
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thaliana DNA
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Pred. No. 1.8e-22;
0; Mismatches 118;
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Quetier,F. and Salanoubat,M.
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PLITSWALSTTECSWTGVTCDVSIRHVTSIDLSGLALSGTLSSDVAHLPLLQNLSIAA
NQISGPIPPQISNLYBELRHLKLSNNVENGSEPDBELSGLNLKVLDLYNNNLTGDLPV
SLTNLTQLRHLHLGGNYFSGKIPATYGTWPVLEYLAVGGNELTGKIPPEIGNLTTULE
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PELEVLQLWENNFTGSIPQEKGRLVLDLSSNKLTGTLPPIMCSGNRLMTLITLG
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CDDVLDSLKEDNIIGKGGAGIYYKGTMPKGDLVAVKRLANTSHGSSHDHGTNAEIQTL
CDDVLDSLKEDNIIGKGGAGIYYKGTMPKGDLVAVKRLANTSHGSSHDHGTNAEIQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana, EMBL:ATU96879; Contains Aminotransferases class-I pyridoxal-phosphate attachment site AA402-415; protein kinases signatures and profile AA812-824; Neutral zinc metallopeptidases, zinc-binding region signature AA928-937*
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DNTLRLWNISSAKFLKTYTGHVNAQYCISSAFSVTNGKRIVSGSEDNCVHMWELNSKK
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DKTIRTYTINTINDPIAEPVQEFTGHENGISDVAFSSDARFIVSASDDKTLKLMDVET
GSLIKTLIGHTNYAFCVNFNPQSNMIVSGSFDETVRIMDVTTGKCLKVLPAHSDPVTA
                                                                                                                                                                                                                                                                          KGLCYLHHDCSPLIVHRDVKSNNILLDSNFEAHVADFGLAKFLQDSGTSECMSAIAGS
YGYIAPEYAYTLKVDEKSDVYSFGVVLLELITGKKPVGEFGDGVDIVQWVRSMTDSNK
                                                                                                                                                                                                                                                                                                                                                            GRIRHRHIVRLLGFCSNHETNLLVYEYMPNGSLGEVLHGKKGGHLHWNTRYKIALEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="receptor protein kinase-like protein"
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/gene="T16K5.20"
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/protein_id="CAB66904.1"
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/gene="T16K5.10"
                                                                                                                                                                                                    QAAESDVTEKAPAINESSPDSGSPPDLLSN"
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/gene="T16K5.10"
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10080. .10166
/gene="T16K5.
                                                                                                                      /gene="T16K5.20"
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                                                                                 'number=
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join(12520. .12645,12721\ .12803,1; 14000. .14131,14223. .14321,14408. 14905. .15017,15108. .15225)

.12803,12885

2885. .13062,13715. .14515,14707. .148

.14802

12520. .15225 /gene="T16K5.30" /gene="T16K5.30" /number=2 /gene="T16K5.20"

0167. .10588 'number=

12645

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/number=10
17693. .17
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GAERMCMPAPTVEQFVEAVTETVLANKRWVPPPGKGSLYVRFLMGTGAVLGLAPAPE
YTFIIYVSPVGNYFKEGVAPIMLIVENEFHRATPGGTGGVKTIGNYAAAGSIAKAKG
SDVLXILDCIYKRYLEEVSSCNIFIVKDNVISTPEIKGTILPGITRKSMIDVARTQGFQ
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/db_xref="GI:6723413"
/translation="MERAAILPSVNONYLLCPSRAFSTRLHSSTRNLSPPSFASIKLQ
HSSSSVSSNGGISLTRCNAVSSNSSSTLYTELADIDWDTVGFGLKPADYMYVNKCNID
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/note="strong similarity to branched-chain-amino-acid
transaminase, Streptomyces coelicolor, PIR:T29053;
Contains Aminotransferases class-IV signature AA292-321"
                                                         /gene="T16K5.30"
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/gene="T16K5.30"
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Best Local Similarity
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         Submitted (01-DEC-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mai lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
                                                                                                                                                                                             1 (bases 1 to 108158)
Bargues,M., Collado,M.C., Navarro,P., Terol,J.,
Mewes,H.W., Lemcke,K., Mayer,K.F.X., Quetier,F.
                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis
AL132978
http://www.genoscope.cns.fr
                                                                                                                              Direct Submission
                                                                                                                                           EU Arabidopsis sequencing, project.
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17693. .18852
/gene="T16K5.40"
join(17693. .17828,17964. .18093,18186. .18852)
/gene="T16K5.40"
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Perez-Alonso, M., and Salanoubat, M.

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7566. A217
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                   /translation="MTKTRILNPTRFPSPKPLRGCGDANFMEQLLHCATAIDSNDAA
LTHQILMVLNNIAPPOGDSTQRLTSAFERALLSRAVSKTPTLSSTISFLPQADELHRF
SVVELAAFVDLTPWHREFETAANAALLTAVEGYSTVHTVDLSLTHCMQLPTLIDAMS
RLNKPPPLLKLTVVSSSDHFPPFINISYEELGSKLVNFATTRNITMEFTIVPSTYSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAGLMSFISAVPESQCPALFQSLLYEACGRTUNPVNGAVGLLMTGNWNVCQAAVETVL
RGGSLKPIPELLNGGGFAGFESPTSDEASEICTEMLNLKADDSGDRNIYHHCRFSSS
RSRRSTASPFKRKRLSEQQPSSELDLSLIPIYPIKTLPFKEDTPSMYSEESVTTVS
FQNNNAGDRYVRCGGGGGGATTKLLNLFA"
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thaliana, EMBL:CAB38293"
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join(11785..11968,12063..12622)
/gene="F3A4.20"
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HRIDQPNPPPSEEEYLALCLLMLARGSSDHHSPPSDHHSLSPLSDHQKDYKCSVCGKS
FPSYQALGGHKTSHRKPVSVDVNNSNGTVTNNGNISNGLVGQSGKTHNCSICFKSFPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="strong similarity to Cys2/His2-type zinc finger protein 1 - Arabidopsis thaliana, EMBL: AB030731; Contains Zinc finger, C2H2 type, domain AA96-116; Zinc finger, C2H2 type, domain AA151-171"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="overlap to BAC number EMBL:AL132965 f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
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19890. .21122
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SSLLQQLRIYPSSFNEALVVNCHMMLRYIPEEPLTSSSSSLRTVFLKQLRSLNPRIV
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/note="Contains Peroxidases signatures AA189-199,Peroxidases signatures AA58-69"
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GAERVERTETKRRWIERMREAEFGGVRVKEDAVADVKAMLEEHAVGWGMKKEDDDESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSKSVEVLQKSQDLLFIAERVELVDRCIDSIAYAICQESQSNEDIVDWWADDLAVLKI
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27649. .2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similarity to non-phototropic hypocotyl 3 - Arabidopsis thaliana, EMBL:AF180390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(24536. .25009,25144. .25632,25686. 26354. .26386))
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LFTDGRSRPTVNAWASNSTAFNRAFVIAMTKLGRVGVKNSSNGNIRRDCGAFN"
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/gene="F3A4.60" complement(27649.

. 28797)

28797

/note="similarity

to several hypothetical proteins

Nagao, K.

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DEFINITION ACCESSION
                                                                                                                                                                                                                                                                                  RESULT 5
YSP972HB/c
                                                                                                                                     SOURCE
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Fission yeast DNA for
D83993
D83993.1 GI:1236271
                                                                                                       chromosome II cosmid 1228 sequence. Schizosaccharomyces pombe (strain:972h-) DNA, cosmid library clone:cosmid 1228.
          {\tt Schizosaccharomycetales:} \ {\tt Schizosaccharomycetaceae:} \\ {\tt Schizosaccharomyces.}
                                                                                Schizosaccharomyces pombe
                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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VNINGFIEEDEEEGOSSRFDDAPEEMDYGYSSFGDSSSSLPAHVRKEILELGYPDDG
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YSVASKTVNVKVQKAIDPEVAALLENSDGSBFGSDVEDLEEDFVVQANLTQKGESSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster, EMBL:AF132172"
/codon <tart-1
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Hfdkapkqflityleercrlsslsinlhsgfpseeftgelspidyhsnssqyiimkif
Hcdglfyctilkdtrivywnpctgqkkwiqtgenldengqdfylgyyqdnkssdksyk
Ilsykgynygdqefkiydiksntwrnldytpipgnyftcsdyryslkgntywfaydlk
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EEEEEEDFMAQEVQNLIHGKAKDYELEEKYMNPADILKNSDSVRDKEEVDTAAHVIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(29810. .31
/note="similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNKMDDETKEMSWRKLFEVEVGTRYYMWSGRPFLVDEEKKIVVCCEKCQKKCQPVITV
SMVEADSNATRVYFPVVTMTSYWPHFVDYVPSLIQIQQSEANEKELNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVEYGENFONGNEDEFVELTEESSDESEKHDCETIVSTYSNLDNLPGKILAAESARQK
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/protein_id="CAB62107.1"
/db_xref="GI:6522920"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(29810.
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/protein_id="CAB62106.1"
/db_xref="GI:6522919"
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AUTHORS
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Submitted (12-MAR-1996) to the DDBJ/EMBL/GenBank databases.
Mitsuhiro Yanagida, Kyoto University, Department of Biophysics;
Kitashirakawa-Oiwakecho, Sakyoku, Kyoto, Kyoto 606, Japan
(E-mail: katayama@kozo.biophys.kyoto-u.ac.jp, Tel:075-753-4205,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 11941)
Yanagida, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
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SDXVSXKETIDSTXSXISLGNIQXXMGALXKXIFHKLGVKATDLGFSNEHDDSQDSLQ
                                                                                                                                                                                          FVQSTPKKMDVSLEDISLDDAALTPIPARMQTPLRKPENNPHTGRSALLHRVLDTNWQ
VQVTPREPKNLQSQEVMDIDSSPFXSPSPISMKMDMPSLNDRNSSHALSLFAEFEHES
YDSINPSGMSPPKTIQFSPHTMGVGSSQQANERSLSLQRKLETLNDSNDSFVKEEDSW
                                                                                                                                                                                                                                                                                                                                                                                         complement(8128. .8790)
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RVMTNLNATVHEVSNSPWQLRPTLSKEFINDNNEVISSIYLLHENGVLQNIIEPAAAR
KRSSLLTALISLGDRKIVLIGDNGDOLQITAEMAACFPERILGIFIRDVMSDECGVL
KXXIXXSXSLPEVVQTKPFATSTPDTPLKEFTTTLKDVDNEQASEFYQLEKEPDTVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDTKAQLNVNVNDGKPNDIELSSTSKTENDPPLSLHTTPDDLQGNGVNVPNPSLSASR
SWYQSGYGISGFFNRINTPSVNSQYISTIGLAKCEEYFEERSLASLQRGLKDEFVLVK
IYATDKNFEQKVVAEFNVPTNVEGYFIIDEVIPFYTTKNNKFSVEAVLLQSTSEDXMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKFSRDVTSSRRKQRKAHFGAPSSVRRVLMSAPLSKELREQYKIRSLPVRRDDQITVIRGSNKGREGKITSVYRKKFLLLIERVTREKANGASAPVGIDASKVUTTKLHLDKDRKDLIVRKGGKVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="putative ribosomal protein L26, most similer
pir: S51347 (68.6% identity in 121 aa overlap)"
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/map="2L between centromere and cdc2"
complement(3855. .4235)
                                                    /protein_id="BAA12200.1"
/db_xref="GI:1827510"
                                                                                                                                                                                                                                                                                              /protein_id="BAA12199.1"
/db_xref="GI:1236275"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGFDVAGYLQSYSLKDWIRIIVYVGGYMLXRPYLMKLGAKIQER
EHRKSLLEGEVDGTLDPEMTHGTKPKEHGEFDTDDDEEEENPDAEFRWGYSARRRIRK
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/translation="MyRFGRLFRGSEESPTINXLTSTTIYPOCFISTGKEYGSEPKH
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ISVHYRGWYYENPDLNNLGRKDRLMLNLLRRYYGLPPKSKETGTYPEKDDENTNLQVY
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                                                                                                    /codon_start=]
                                                                                                                           /note="unnamed
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/db_xref="GI:1236274"
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/strain="972h-"
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                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4235 ATGAAGTTCTCCAGGGATGTCACTAGCTCTCGTCGCAAGCAGAAAAGGCTCACTTCGGC 4176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGAGCGTGTCACCCGCGAGAAGGCCAACGGTGCCTCTGCACCCGTCGGTATCGACGCC
                                                                                                                                                                                                                                                                                          AL391603.1 GI:9929282 60s ribosomal protein L26; atfl; isp4; sexual differentiation; transription factor. fission yeast.
                                                     Submitted (24-AUG-1999) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.
Notes:
Details of yeast sequencing at the Sanger Centre are available
                                                                                                                                Wood, V., Rajandre
                                                                                                                                                                                                   Schizosaccharomyces
                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota;
Schizosaccharomycetales; Schi
                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe
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LVCVQTSTAETFXSVDRELTTYDLNTIKILXTAPSFTAQNWLFIMHHLEIVGYLFPHX
AHLDKQYSLLDYAKSVEHXPELGTVQRKGFEEQSRI"
AHLDKQYSLLDYAKSVEHXPELGTVQRKGFEEQSRI"
ALDKQYSLLDYAKSVEHXPELGTVQRKGFEEQSRI"
ALDKQYSLLDYAKSVEHXPELGTVQRKGFEEQSRI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA12201.1"
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                                                                                                                                                   Rajandream, M.A., Barrell, B.G., Saunders, D. and Harris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                         14147 bp DNA
omosome II cosmid
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Pred. No. 6.4e-21;
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                                                                                                                                                                                                                           Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 c29B5
                                                                                                                                                                                                                                                 Schizosaccharomycetes;
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During 1995 to 1996 about 66% of S. pombe chromosome 1 was sequenced by the Sanger Centre. The sequencing of the S. pombe sequenced by the Sanger Centre. The sequencing of the S. pombe genome is now being continued with funding from The European genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project.

Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in Pombase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.

CDS are numbered using the following system eg SBBC25H2.01c. SP (S. pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are also included but some of these may be fortuitous. The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for overlapping sections once, or longer, because we arrange for overlapping sections once, or longer, because we arrange for overlapping sections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the World Wide Web.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overlap between neighbouring submissions.
d c29B5 is overlapped at the 3' end by cosmid c27, EMBL entry
7, accession number Al353866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="transcription factor atf1"
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/product="transcription factor atf1"
/product="transcription factor atf1"
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AFTRGTMHNPLSPAIVDATLREDYLNNPSDASAAARFSSGTGFTPGVNEPFRSLLTPT
GAGFPAASSGTANLLGPHTFDSQFPDQYRFTPBRDGKPPVVNGTNCDQSDYFGANAAVH
GLCLLSQVPDQQOKLQQPISSENDQAASTTANNLLKQTQQOTFPDSIRPSFTQNINPQ
AVTGTMNPQASSTQQQPMYFMGSQQFNGMPSVVGDTVNPADPSLTLRQTTDFSGONAE
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                                                                                                                                                                                                                                                                                                                                                                                                            /note="Match
Score 48.62"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="nominal overlap with SPBC83 S.
224. .1924
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/db_xref="GI:9955814"
                                                                                                                                                                                                                                                              complement(2997. .5354)
                                                                                                                                                                                                                                                                                                                                                                       complement(2997. .5354)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="atfl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="mts1; sss1; gad7; SPBC29B5.01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="cosmid c29B5"
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/chromosome="II"
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                                                                                                                                                                                                                     /gene="isp4
                                                                                                                                                                                                                                                                                                                                  /gene="isp4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="atf1"
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                                                                                                                                                                                   /note="SPBC29B5.02c, len:786"
                                                                                                                                                                                                                                                                                                /note="SPBC29B5.02c"
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BASE COUNT
ORIGIN
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Best Local
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                                                        11183 ATGAAGTTCTCCAGGGATGTCACTAGCTCTCGTCGCAAGCAGAGAAAGGCTCACTTCGGC 11124
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96
                                                                                            atgaagtattccaaagttgtatcgtcgtctagaagaagcagagggaaagcatactttcaa 155
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                                                                                                                                                                               Conservative
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13995. .14147
/notce="nominal overlap with SPBC27 S. pombe
2724 c 2550 g 4300 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein similar to yeast YNL094W"
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/db_xref="G1:9955816"
/tanslation="kersegriferesesptindltsTriypocfistckeygsepkh
ISVHVRGWVYENPDLNNLGRKDRLMLNLLRRYVGLPPKSKETGTYPEKDDENTNLQVV
VDTKAQLNVNVNDGKENDIELSSTSKTENDPPLSLHTTPDDLQGNGVNVPNPSLSASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRSSLLTAIRSLGDRKIVLIGDNGEQDLQIYAEMAACFPERILGIFIRDVMSDFCGVL
KKQTTKSNSLPEVVQTKPFATSTPDTPLKEFTTTLKDVDNEQASEFYQLEKEPDTVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAYMSEVPVLDRNGISIISDIDDTVKNTRVIEGPRKVGETTLLAPLNTQTIEGVSDWF
RVMTNLNATVHFVSNSPWQLWPTLSKFFTNDNMPYISSIYLRHFNGVLQNIIEPAAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWYQSGYGISGFFNRIMTPSVNSQYISTIGLAKCEEYFEERSLASLQRGLKDEFYLVK
IYATDKNFEQKVVAEFNVATNVEGYFIIDEVIPFYTTKNNKFSVEAVLLQSTSEDKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(11868. .13685)
/gene="SPBC29B5.04c"
/note="SPBC29B5.04c, len:606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(10866. .11039)
/gene="rpl26"
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GYIPPATPVNYLAWSGIGLFFNYYLKKIFADWWQKYNFTLSAALDTGTQLSVIILFFC
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KLPPRIMFYTQMIATIWSCFVQIGVLDWALGNIDNVCQADQPDNYTCPNATVFFNSSV
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ATFDLDAYQNYSPIFMSTTYALAFGLSFASITSVIFHVILYHGKEIYDRLRDPPAPDI
HEKLMKAYDEVPFYWYLSVFLAFFGMMMGTIYGWKTETPWWVIIVGVIFSAVWEIPIG
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TVGAAVNMFFSLRVEHTLSVLISELLAYPALOIWDLIFDDREFETIGRIKENTKPEPF
TVKEHALIVMSSVSFGNAYSTDIILAQRVHYKQRFGFGYEICLTLATQLIGYGLAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(11868. .13685)
/gene="SPBC29B5.04c"
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RSLPVRRDDQITVIRGSNKGREGKITSVYRKKFLLLIERVTREKANGASAPVGIDASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="60s ribosomal protein 126"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(10803. .11183)
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WFPSYIFQALSLFAWVTWIRPNSPTVNQIFGESTGISILPMTFDWNQISAYILSPLMA
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/note="region of unusual composition"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5478
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(bases 1 to 97911)
Myler,P.J., Sisk,E., Cawthra,J., Nelson,S., Vogt,C., Robertson,L.,
McDonagh,P., Ivens,A., Nguyen,D., Munden,H., Stuart,K., Mack,J.,
Marty,A. and Seyler,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-JUN-2001) Seattle Biomedical Research Institution, Nickerson Street, Seattle, WA 98109-1651, USA On Jun 9, 2001 this sequence version replaced gi:13811913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-APR-2001)
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/chromosome="35"
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/strain="Friedlin"
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of Saccharon
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STS.
                                                                                                                                                                                                                                                                                                                 Submitted (07 SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zgosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolottin Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1)
TEBS Lett. 487 (1), 3-12 (2000)
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Souciet, J.L., Aigle, M., Artiquenave, F., Blandin, G.
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FEBS Lett. 487 (1), 37-41 (2000)
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                           /db_xref="taxon:4931"
/clone="ASOAA019H06"
/clone_lib="ASOAA"
/note="end_: T7"
                                                                                                         /note=" <528. .
                 /note="similar to Saccharomyces cerevisiae ORF YGR034w
RPL26B; 60S large subunit ribosomal protein ]"
/evidence=not_experimental
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168 c 186 g 286 t 2 others
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                                                                                                                             TTATATAGACGTTTCTTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATC 1035
AGGTTCTGAAGGTAAAGTTAATTCTGTTTATAGATTGAAATTTGCTATTCAAGTTGATAA 1215
                gggtagagaaggaaagttacaacgtgttatcgaaagaaatatcgggatacatatcgagag 343
                                                                       cgttcgttctttacctattcgaaaagaagacgaagtaatcatagttcgcggagctttcaa 283
                                                                                                              AGTTGAAAGAAGAGTTCTTTTATCTGCTCCATTATCCAAAGAATTAAGACAACAATACAA 1095
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Sequence 409
AX073298
AX073298.1
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cell death related drug targets in yeast and Patent: WO 0102550-A 409 11-JAN-2001;

JANSSEN PHARMACEUTICA N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans.
Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota;
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                                                                                                                                                                                                                                     Similarity
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409 from Patent W00102550.
                                                                                                                                                                                                                                                                                                           /organism="Candida albicans"
/db_xref="taxon:5476"
194 c 196 g 446 t
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1e-18;
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1.1e-18;
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                   278 TCCTCTGGACAATCCGTTCCCCTCGGTATCCACCCATCCAAGGTCATCA 326
                                                                                                                                        158
                                                                                                                                                                                                                                                              120 tcgtctagaagaaagcagaggaaagcatactttcaagcaccatcttctgtacgacgaata 179
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                                    gcgaatggaatgactgtacctgtgggaatacatccatctaatgttgtta 408
                                                                                          9ttacaacgtgttatcgaaaagaaatatcggatacatatcgagagagtgaccagagaaaaa 359
                                                                                                                               ATCAGAAAGGATGATGAGGTCACCATCGTTCGTGGTTCCAACAAGGGCTCCGAGGGAAAG
                                                                                                                                                  attogaaaagaagacgaagtaatcatagttogoggagctttoaagggtagaggaaggaaaa 299
                                                                                                                                                                                      ATCATGAGCGCTCCTTTGAGCAAGGAACTCCGTGAGAAGTACAACGTCCGCTCCATCCCA 157
                                                                                                                                                                                                         ATCACCTCCGTCTACCGTCTCAAATACGTCGTCCACGTCGAGCGTGTCGTCAAGGAGAAG
                                                                                                                                                                                                                                               TCCTCCAGGAGAAAGTCCCGCAAGGCTCATTTCGATGCCCCATCCAGCGTCAGACGTACC 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library; nitrogen deprivation.
Botryotinia fuckeliana
Botryotinia fuckeliana
Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-SEP-1999) Phytopathologie,
78026 Versailles, France
2 (bases 1 to 480)
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Bitton, F., Levis, C.,
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                                                                                                                                                                                                                                                                                                                                                                                               132
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                                                                                                                                                                                                                                                                                                                                                                                         /note="Genoscope sequence ID : W24A111" 128 c 116 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="T4"
/db_xref="taxon:40559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Botryotinia fuckeliana"
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Pred. No. 8.1e-18;
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             Botrytis cinerea strain nitrogen deprivation. AL111303 AL111303.1 GI:5825922
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Direct Submission
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Botryotinia fuckeliana
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Botrytis cinerea strain
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library; nitrogen
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                                                       cinerea strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Genoscope sequence
138 c 119 g 109
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/strain="T4"
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deprivation
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120 tcgtctagaagaaagcagaggaaagcatactttcaagcaccatcttctgtacgacgaata 179
                                                                                                                                                          gcgaatggaatgactgtacctgtgggaatacatccatctaatgttgtta 408
                                                                                                                                                                                                                                                                                                                                                                                                ATCATGAGCGCTCCTTTGAGCAAGGAACTCCGTGAGAAGTACAACGTCCGCTCCATCCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTCTGGACAATCCGTTCCCCTCGGTATCCACCCATCCAAGGTCATCA
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                                                                                                                                                                                                                                                                                                                                        attcgaaaagaagaagtaatcatagttcgcggagctttcaagggtagagaaggaaaa 299
                                                                                                                                                                                                                     ATCACCTCCGTCTACCGTCTCAAATACGTCGTCCACGTCGAGCGTGTCGTCAAGGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grunder conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plan The library was produced in an oriented direction, in the pBSII
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The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its bost patients.
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Botryotinia fuckeliana
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Eukaryota; Fungi; Ascomycota; Pezi;
Helotiales; Sclerotiniaceae; Botryy
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Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y
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The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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CP 5706 91057 EVRY cedex - FRANCE (E-mail: seqref@genoscope.c - Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Bottytis cinerea strain which was under conditions of nitrogen deprivation, which is the normal
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 tegtetagaagaaageagaaggaaageataettteaageaeeatettetgtaegaegaata 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 ATCAGAAAGGATGATGAGGTCACCATCGTTCGTGGTTCCAACAAGGGCTCCGAGGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ATCATGAGCGCTCCTTTGAGCAAGGAACTCCGTGAGAAGTACAACGTCCGCTCCATCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 attegaaaagaagacgaagtaateatagttegeggagettteaagggtagagaaggaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 TCCTCCAGGAGAAAGTCCCGCAAGGCTCATTTCGATGCCCCATCCAGCCGTCAGACGTACC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCTGGACAATCCGTTCCCCTCGGTATCCACCCATCCAAGGTCATCA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCACCTCCGTCTACCGTCTCAAATACGTCGTCCACGTCGAGCGTGTCGTCAAGGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gttacaacgtgttatcgaaagaatatcggatacatatcgagagagtgaccagagagaaaaa
                                                                                                                    The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
                                                                                                                                                                                                                                                                                                                   Eukaryota; Fung; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases 1 to 540)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 540)
                                                                                                                                                                                                                                      Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL114653.1 GI:5829272
CDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
                                                                                                                  The library was produced in an oriented direction, vector.
                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Botrytis cinerea strain nitrogen deprivation.
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                 /organism="Botryotinia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
                                                                                            Location/Qualifiers
/note="Genoscope sequence
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146 c 128 g 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 106.6; DB Pred. No. 8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA PLN
T4 cDNA library under
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 ID : W62D111"
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   293
                                            233 ATCACCTCCGTCTACCGTCTCAAATACGTCGTCCACGTCGAGCGTGTCGTCAAGGAGAAG
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                                                                                                                                          113 ATCATGAGCGCTCCTTTGAGCAAGGAACTCCGTGAGAAGTACAACGTCCGCTCCATCCCA 172
                                                                                                                                                                        180
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TCCTCTGGACAATCCGTTCCCCTCGGTATCCACCCATCCAAGGTCATCA 341
                                                            gttacaacgtgttatcgaaagaaatatcggatacatatcgagagagtgaccagagaaaaa
                                                                                            ATCAGAAAGGATGATGAGGTCACCATCGTTCGTGGTTCCAACAAGGGCTCCGAGGGAAAG
                                                                                                        attogaaagaagacgaagtaatcatagttogoggagotttoaagggtagagaaaggaaaa
                                                                                                                                                        TCCTCCAGGAGAAAGTCCCCGCAAGGCTCATTTCGATGCCCCATCCAGCGTCAGACGTACC 112
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60.6%;
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Search completed: March Job time: 3221 sec 2, 2002, 20:57:16